Performance Check

GeneMapper® *ID-X* Version 1.4

The following report verifies the performance of the Applied Biosystems GeneMapper ID-X Version 1.4 Software.

GMID-X v1.4 is approved for use on 2/1/15.

2/1/15

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I. Introduction

This report describes a performance check of the Applied Biosystems GeneMapper® *ID-X* Version 1.4 Software. It demonstrates the laboratory's adherence to Standard 8.7 of the Quality Assurance Standards for DNA Testing Laboratories which states:

"Modifications to software, such as an upgrade, shall require a performance check prior to implementation. New software or significant software changes that may impact interpretation or the analytical process shall require a validation prior to implementation."

It also demonstrates the laboratory's adherence to the SWGDAM Validation Guidelines, Section 7.2, which states:

"A software upgrade that would not impact interpretation, the analytical process, or sizing algorithms shall require a performance check."

II. Performance Check

a. Objective

Samples will be analyzed in both GeneMapper® *ID-X* Version 1.3 and GeneMapper® *ID-X* Version 1.4. Allele calls, peak heights and base pair sizes will be evaluated to confirm concordance. In addition, all panels, bin sets and stutter files will be compared to verify concordance.

b. Materials and Methods

GeneMapper® *ID-X* Version 1.3

Analysis Method:	Identifiler_Plus_AnalysisMethod_v1X (PAT = 70rfu)
Panel:	Identifiler_Plus_Panels_v1X
Bin Set:	Identifiler_Plus_Bins_v1X
Stutter File:	AmpFLSTR_Stutter_v1X
Size Standard:	CE_G5_HID_GS500

GeneMapper® *ID-X* Version 1.4

Analysis Method:	Identifiler_Plus_AnalysisMethod_v1X (PAT = 70rfu)
Panel:	Identifiler_Plus_v1.2X
Bin Set:	AmpFLSTR_Bins_v3X
Stutter File:	AmpFLSTR_Stutter_v3X
Size Standard:	CE_G5_HID_GS500

Run used for analysis:

Plate Name:	061314JS-RUN1
Injections:	1_Run_3130xl_MPD_2014-06-13_07-21_1312
	2_Run_3130xl_MPD_2014-06-13_10-55_1313
Samples:	1_A03_LADDER_1312_001.fsa
	1_B03_10-573-JS-COMP-1_1312_003.fsa
	1_C03_10-573-JS-COMP-2_1312_005.fsa
	1_D03_060914JS-RRB1_1312_007.fsa
	1_E03_061214JS-POS1_1312_009.fsa
	1_F03_061214JS-NEG1_1312_011.fsa
	2_A01_LADDER_1313_001.fsa

2_A02_060514JS-RB1SF_1313_002.fsa
2_B01_10-573-JS-COMP-3-1_1313_003.fsa
2_B02_061214JS-POS1_1313_004.fsa
2_C01_060614JS-RB1_1313_005.fsa
2_C02_061214JS-NEG1_1313_006.fsa
2_D01_10-573-JS-COMP-4-1EF1_1313_007.fsa
2_D02_LADDER_1313_008.fsa
2_E01_060514JS-RB1EF1_1313_009.fsa
2_F01_10-573-JS-COMP-4-1EF2_1313_011.fsa
2_G01_060514JS-RB1EF2_1313_013.fsa
2_H01_10-573-JS-COMP-4-1SF_1313_015.fsa

c. Experimental Setup/Data Analysis

The above listed samples were analyzed in GeneMapper® *ID-X* Version 1.3 using the parameters listed above. They were also analyzed in GeneMapper® *ID-X* Version 1.4 with the parameters listed above. Each electropherogram was printed and a combined table was exported. All allele calls, base pair sizes and peak heights were evaluated by two separate individuals to confirm concordance.

The different panels, bin sets and stutter files were also exported and printed. Each value was compared and evaluated by two separate individuals to confirm concordance.

d. Results

See electropherograms and printed tables.

All allele calls, peak heights and base pair sizes were verified by DFS Intern Maurice Griffin and Forensic Scientist III Jessica Skillman. All values were determined to be concordant.

All values in the panels, bin sets and stutter files were verified by DFS Intern Maurice Griffin and Forensic Scientist III Jessica Skillman. All values were determined to be concordant.

e. Conclusions

The GeneMapper® *ID-X* Version 1.3 software produced concordant results with the GeneMapper® *ID-X* Version 1.4 software. The GeneMapper® *ID-X* Version 1.4 software is recommended for use in casework analysis for the purpose of analyzing samples and printing electropherograms for interpretation.

III. Appendix – Setup worksheet, electropherograms and data tables